Sequence Search Summary with SEQ ID NO:1 in DNA databases

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 17:35:39 ; Search time 3098 Seconds
                                          (without alignments)
                                          10605.897 Million cell updates/sec

Title: US-09-941-945A-1
Perfect score: 1129
Sequence: 1 catatgcaggcgaactcctg..........ccagtggaatccacttcgga 1129

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1:   gb_ba:*
                 2:   gb_htg:*
                 3:   gb_in:*
                 4:   gb_om:*
                 5:   gb_ov:*
                 6:   gb_pat:*
                 7:   gb_ph:*
                 8:   gb_pl:*
                 9:   gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

*Also searched SEQ ID NO:2
(the encoded amino acid seq)
in DNA databases*

→ same hits found

```
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID		Description
	1	1129	100.0	328050	1	AP005275	*Nakagawa*	AP005275 Corynebac
	2	1129	100.0	349980	6	AX127144	*EP 1108790*	AX127144 Sequence
	3	1129	100.0	349980	6	AX127145	"	AX127145 Sequence
	4	564	50.0	564	6	AX120753		AX120753 Sequence
	5	263	23.3	1026	6	AX120754		AX120754 Sequence
	6	133.4	11.8	874	6	AR199611		AR199611 Sequence
c	7	133.4	11.8	14240	1	AE007157		AE007157 Mycobacte
c	8	133.4	11.8	33818	1	MTCY78		Z77165 Mycobacteri
	9	83.2	7.4	31624	1	SCD63		AL161755 Streptomy
	10	80.2	7.1	4692	1	SCAJ10601		AJ010601 Streptomy
c	11	62.4	5.5	42325	1	U00015		U00015 Mycobacteri
	12	62.4	5.5	344050	1	MLEPRTN2		AL583918 Mycobacte
c	13	43	3.8	125020	9	AF429315		AF429315 Homo sapi
	14	42.8	3.8	125020	9	AF429315		AF429315 Homo sapi
	15	42	3.7	199863	2	AC124172		AC124172 Mus muscu
	16	41.8	3.7	176547	2	AC126433		AC126433 Mus muscu
	17	41.8	3.7	236404	2	AC117241		AC117241 Mus muscu
	18	39.4	3.5	36144	1	SC9C5		AL357523 Streptomy
	19	39.4	3.5	38640	1	SCL2		AL137778 Streptomy
	20	38.8	3.4	5610	6	AX278007		AX278007 Sequence
	21	38.8	3.4	5610	6	AX280000		AX280000 Sequence
	22	38.8	3.4	5610	6	AX281189		AX281189 Sequence
	23	38.8	3.4	5610	6	AX323704		AX323704 Sequence
	24	38.8	3.4	5610	6	AX356456		AX356456 Sequence
	25	38.4	3.4	193047	9	CNS0000Q		AL049874 Human chr
	26	38	3.4	2070	1	SCO010584		AJ010584 Streptomy
	27	38	3.4	38084	1	SCE68		AL079345 Streptomy
c	28	38	3.4	179138	9	CNS07EGV		AL606834 Human chr
	29	37.8	3.3	18011	6	AX344937		AX344937 Sequence
	30	37.4	3.3	172746	2	AC025279		AC025279 Homo sapi
c	31	37.4	3.3	174010	2	AC023814		AC023814 Homo sapi
	32	37.4	3.3	177130	3	AC092219		AC092219 Drosophil
c	33	37.4	3.3	179529	2	AC020004		AC020004 Drosophil

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 16:24:33 ; Search time 325 Seconds
                                           (without alignments)
                                           7823.096 Million cell updates/sec

Title: US-09-941-945A-1
Perfect score: 1129
Sequence: 1 catatgcaggcgaactcctg..........ccagtggaatccacttcgga 1129

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_101002:*
                   1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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                   20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
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                   22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                   23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                   24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

```
                            SUMMARIES
                      %
Result              Query
   No.   Score   Match Length DB  ID                  Description
-----------------------------------------------------------------------
      1   1129   100.0 349980 22  AAH68525  EP1108790  C glutamicum codin
      2   1129   100.0 349980 22  AAH68526    "    "   C glutamicum codin
      3  1125.8   99.7   1129 24  ABA96000 -App's DE doc  Corynebacterium gl
      4    564    50.0    564 22  AAH65634            C glutamicum codin
      5    263    23.3   1026 22  AAH65635            C glutamicum codin
      6   133.4   11.8   1105 19  AAV44589            Mycobacterium tube
 c    7   133.4   11.8 4403765 22  AAI99683            Mycobacterium tube
 c    8   133.4   11.8 4411529 22  AAI99682            Mycobacterium tube
      9    38.8    3.4   5610 22  AAS45462            Chemically pretrea
     10    38.8    3.4   5610 24  ABL92281            Chemically treated
     11    38.8    3.4   5610 24  ABL49354            Human polynucleoti
     12    38.8    3.4   5610 24  AAD22332            Chemically treated
     13    38.8    3.4   5610 24  ABK28318            DNA transcription
     14    37.8    3.3  18011 24  ABL32035            Human immune syste
     15    37.4    3.3   2322 23  ABL28721            Drosophila melanog
 c   16    37.4    3.3   4471 23  ABL28720            Drosophila melanog
     17    37.2    3.3    950 22  AAK84920            Human immune/haema
     18    37.2    3.3   4397 22  AAK84921            Human immune/haema
     19    35.4    3.1   1110 21  AAC45795            Arabidopsis thalia
     20    35.4    3.1   1380 21  AAC37623            Arabidopsis thalia
     21    35.4    3.1   1429 19  AAV04237            Arabidopsis C-14 s
 c   22    35      3.1   4639 24  ABK83705            Human cDNA differe
 c   23    35      3.1   5924 22  AAI59245            Human polynucleoti
 c   24    35      3.1   5925 22  AAI61031            Human polynucleoti
     25    34.6    3.1   8996 22  AAS45504            Chemically pretrea
     26    34.6    3.1   8996 24  ABK28436            DNA transcription
 c   27    34.4    3.0   1401 19  AAV34002            S. peucetius dnrX
 c   28    34.4    3.0   2828 21  AAA93121            Human secreted pro
 c   29    34.2    3.0   1590 22  AAI71949            Thermus caldophilu
     30    34      3.0    566 24  ABQ60238            Human colon cancer
     31    33.8    3.0   1420 21  AAZ90582            Maize SINA ortholo
     32    33.8    3.0   1428 21  AAC43673            Zea mays DNA fragm
     33    33.8    3.0  14649 22  AAS45415            Chemically pretrea
     34    33.8    3.0  14649 24  ABK28268            DNA transcription
     35    33.6    3.0  89328 24  ABL61995            Colon adenocarcino
 c   36    33.4    3.0    365 22  AAK17670            Human brain expres
 c   37    33.4    3.0    365 22  AAI24269            Probe #14202 for g
 c   38    33.4    3.0    852 21  AAC55802            S. lavendulae MitM
     39    33.4    3.0    935 21  AAC00969            Human secreted pro
 c   40    33.4    3.0   5581 19  AAV17098            Human pancreatic c
     41    33.4    3.0  53500 21  AAC55842            Complete nucleotid
     42    33.2    2.9    501 24  ABQ42772            Oligonucleotide fo
 c   43    33.2    2.9    501 24  ABQ42773            Oligonucleotide fo
     44    33.2    2.9  10713 24  ABL32741            Human immune syste
     45    33      2.9    700 22  AAH92867            Human inflammatory
```

ALIGNMENTS

RESULT 1

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 19:37:19 ; Search time 303 Seconds
                                           (without alignments)
                                           7686.891 Million cell updates/sec

Title: US-09-941-945A-1
Perfect score: 1129
Sequence: 1 catatgcaggcgaactcctg..........ccagtggaatccacttcgga 1129

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
                 11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq3:*
                 13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description
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      1   1129   100.0   1129 11   US-09-941-945A-1   Sequence 1, Appli

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     2    1129  100.0  3309400  11   US-09-738-626-1        Sequence 1, Appli
     3     564   50.0      564  11   US-09-738-626-669      Sequence 669, App
     4     263   23.3     1026  11   US-09-738-626-670      Sequence 670, App
     5      84    7.4  9025608  15   US-10-156-761-1        Sequence 1, Appli
     6    81.6    7.2      573  15   US-10-156-761-4983     Sequence 4983, Ap
     7    38.8    3.4     5610  15   US-10-239-676-170      Sequence 170, App
     8    38.4    3.4     2320  15   US-10-027-632-264352   Sequence 264352,
     9    36.4    3.2      671  15   US-10-184-644-346      Sequence 346, App
    10    36.4    3.2      671  15   US-10-184-634-346      Sequence 346, App
c   11    35.6    3.2      453  11   US-09-938-842A-3437    Sequence 3437, Ap
    12    35.4    3.1     1429   8   US-08-879-337-1        Sequence 1, Appli
    13      35    3.1      716  14   US-10-146-731-96       Sequence 96, Appl
    14      35    3.1      716  15   US-10-123-155-96       Sequence 96, Appl
    15    34.6    3.1     8996  15   US-10-239-676-212      Sequence 212, App
    16    34.4    3.0      414  15   US-10-184-644-314      Sequence 314, App
    17    34.4    3.0      414  15   US-10-184-634-314      Sequence 314, App
    18    34.4    3.0      858  15   US-10-156-761-6230     Sequence 6230, Ap
c   19    34.4    3.0     1506  15   US-10-156-761-5159     Sequence 5159, Ap
    20    34.4    3.0     2617  15   US-10-027-632-262422   Sequence 262422,
    21    34.4    3.0     5234  15   US-10-027-632-262421   Sequence 262421,
    22    33.8    3.0    14649  15   US-10-239-676-122      Sequence 122, App
c   23    33.6    3.0      333  11   US-09-960-352-12655    Sequence 12655, A
c   24    33.4    3.0      365  10   US-09-864-761-27103    Sequence 27103, A
c   25    33.4    3.0      693  15   US-10-156-761-1183     Sequence 1183, Ap
c   26    33.4    3.0      852  15   US-10-267-255-36       Sequence 36, Appl
c   27    33.4    3.0     1539  15   US-10-156-761-75       Sequence 75, Appl
c   28    33.4    3.0     5581  15   US-10-087-993-33       Sequence 33, Appl
    29    33.4    3.0    53500  15   US-10-267-255-76       Sequence 76, Appl
c   30    33.4    3.0  9025608  15   US-10-156-761-1        Sequence 1, Appli
c   31    33.2    2.9     1155  15   US-10-156-761-1636     Sequence 1636, Ap
c   32    32.8    2.9      424  11   US-09-867-701-3179     Sequence 3179, Ap
c   33    32.8    2.9     1049  14   US-10-146-731-358      Sequence 358, App
c   34    32.8    2.9     1049  15   US-10-123-155-358      Sequence 358, App
c   35    32.8    2.9     1533  15   US-10-156-761-779      Sequence 779, App
c   36    32.8    2.9     1805  10   US-09-823-114-18       Sequence 18, Appl
c   37    32.8    2.9     1805  15   US-10-290-748-18       Sequence 18, Appl
c   38    32.8    2.9     1829  12   US-09-905-186A-7       Sequence 7, Appli
c   39    32.8    2.9     1829  12   US-09-905-186A-8       Sequence 8, Appli
c   40    32.8    2.9     1829  12   US-09-905-186A-9       Sequence 9, Appli
c   41    32.8    2.9     1829  12   US-09-905-186A-10      Sequence 10, Appl
c   42    32.8    2.9     1829  12   US-09-905-186A-11      Sequence 11, Appl
c   43    32.8    2.9     2534  15   US-10-087-345A-22      Sequence 22, Appl
c   44    32.8    2.9     2534  15   US-10-225-567A-208     Sequence 208, App
c   45    32.8    2.9     2602  12   US-09-905-186A-1       Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-09-941-945A-1
; Sequence 1, Application US/09941945A
; Patent No. US20020111468A1
; GENERAL INFORMATION:
; APPLICANT: BATHE, Brigitte, et al.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE sigD GENE
; FILE REFERENCE: 032301 WD 190

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 18:13:17 ; Search time 1896 Seconds
                                          (without alignments)
                                          9643.832 Million cell updates/sec

Title: US-09-941-945A-1
Perfect score: 1129
Sequence: 1 catatgcaggcgaactcctg..........ccagtggaatccacttcgga 1129

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                  1: em_estba:*
                  2: em_esthum:*
                  3: em_estin:*
                  4: em_estmu:*
                  5: em_estov:*
                  6: em_estpl:*
                  7: em_estro:*
                  8: em_htc:*
                  9: gb_est1:*
                  10: gb_est2:*
                  11: gb_htc:*
                  12: gb_est3:*
                  13: gb_est4:*
                  14: gb_est5:*
                  15: em_estfun:*
                  16: em_estom:*
                  17: gb_gss:*
                  18: em_gss_hum:*
                  19: em_gss_inv:*
                  20: em_gss_pln:*
                  21: em_gss_vrt:*
                  22: em_gss_fun:*
                  23: em_gss_mam:*
                  24: em_gss_mus:*
                  25: em_gss_other:*
                  26: em_gss_pro:*
                  27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	45.2	4.0	1207	17	CNS015ZN	AL106109 Drosophil
c	2	39	3.5	1101	17	CNS00LO0	AL068607 Drosophil
c	3	39	3.5	1101	17	CNS00ZB7	AL097453 Drosophil
	4	38.6	3.4	1101	17	CNS00LT2	AL078714 Drosophil
	5	37.6	3.3	2072	11	AK016917	AK016917 Mus muscu
c	6	37.2	3.3	435	14	W96254	W96254 ze42b01.r1
c	7	37.2	3.3	444	9	AA018279	AA018279 ze53h06.r
c	8	37.2	3.3	460	9	AA018267	AA018267 ze53g07.r
c	9	37.2	3.3	464	9	AA054016	AA054016 zf48h07.r
c	10	37.2	3.3	493	9	AA013384	AA013384 ze28b12.r
c	11	37.2	3.3	505	14	H86191	H86191 ys94g06.r1
	12	37.2	3.3	807	12	BG321006	BG321006 Zm04_03e1
	13	37.2	3.3	887	13	BI096866	BI096866 SCUMtig11
c	14	37	3.3	389	14	H84094	H84094 ys94f11.r1
c	15	37	3.3	400	14	H84088	H84088 ys94e12.r1
c	16	37	3.3	427	9	AA056119	AA056119 zf55g07.r
	17	36.8	3.3	1101	17	CNS00FCQ	AL070525 Drosophil
c	18	36.6	3.2	421	17	AQ234900	AQ234900 HS_2054_A
c	19	36.6	3.2	475	12	BF412036	BF412036 UI-R-BT1-
c	20	36.6	3.2	704	17	AG171291	AG171291 Pan trogl
	21	36.6	3.2	884	17	CNS006U0	AL065923 Drosophil
	22	36.4	3.2	289	10	AW372518	AW372518 PM3-BT034
c	23	36.4	3.2	541	17	AQ611746	AQ611746 HS_5087_B
c	24	36.4	3.2	565	17	B68684	B68684 CIT-HSP-205
c	25	36.2	3.2	706	13	BM338529	BM338529 MEST228-C
	26	36.2	3.2	797	13	BI829416	BI829416 603080434
	27	36	3.2	1101	17	CNS0100X	AL098379 Drosophil
	28	35.8	3.2	482	17	P752L	AL354014 Leishmani
	29	35.8	3.2	498	17	P332R	AL160657 Leishmani
c	30	35.8	3.2	602	14	BQ200778	BQ200778 UI-R-EB1-
c	31	35.8	3.2	939	17	CNS00CNG	AL059400 Drosophil
	32	35.6	3.2	240	10	BB012808	BB012808 BB012808
c	33	35.6	3.2	895	12	BF166253	BF166253 601777016
	34	35.4	3.1	454	10	AV619431	AV619431 AV619431
c	35	35.4	3.1	506	10	AW308983	AW308983 sf92f04.y
	36	35.4	3.1	591	14	W44028	W44028 mc72g12.r1
	37	35.4	3.1	692	17	BH453605	BH453605 BOHJS75TF
c	38	35.2	3.1	412	17	BH757495	BH757495 SALK_0563
	39	35.2	3.1	543	13	BM330956	BM330956 PIC1_67_F
	40	35.2	3.1	555	13	BM330963	BM330963 PIC1_67_G
	41	35.2	3.1	579	13	BM331661	BM331661 PIC1_59_D
	42	35.2	3.1	582	13	BM318188	BM318188 PI1_79_E0
c	43	35.2	3.1	584	12	BF042140	BF042140 BP250023A
c	44	35.2	3.1	594	12	BF042242	BF042242 BP250021B
	45	35.2	3.1	597	10	BE598653	BE598653 PI1_84_A0

ALIGNMENTS

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 18:29:46 ; Search time 71 Seconds
                                            (without alignments)
                                            4876.592 Million cell updates/sec

Title: US-09-941-945A-1
Perfect score: 1129
Sequence: 1 catatgcaggcgaactcctg..........ccagtggaatccacttcgga 1129

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                   1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                   2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                   3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                   4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                   5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                   6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                         %
Result   Query
    No.   Score   Match Length DB   ID   Description
    ----
       1   133.4   11.8   874 4   US-09-082-920-1   Sequence 1, Appli
 c   2   133.4   11.8 4403765 4   US-09-103-840A-2   Sequence 2, Appli
 c   3   133.4   11.8 4411529 4   US-09-103-840A-1   Sequence 1, Appli
 c   4   34.8   3.1   771 4   US-09-221-017B-667   Sequence 667, App
 c   5   34.4   3.0   1401 2   US-08-812-412-1   Sequence 1, Appli
 c   6   34.4   3.0   1401 4   US-09-180-271-4   Sequence 4, Appli
 c   7   34.2   3.0   7218 1   US-08-232-463-14   Sequence 14, Appl
       8   33.8   3.0   1420 3   US-09-362-506-1   Sequence 1, Appli
 c   9   32.8   2.9   1805 4   US-08-405-271A-18   Sequence 18, Appl
      10   32.6   2.9   2588 2   US-08-796-414B-6   Sequence 6, Appli
 c   11   32.6   2.9   30001 1   US-08-125-468-1   Sequence 1, Appli